ABSTRACT

Disclosed is a method for determining whether a dog is an extensive metabolizer or a poor metabolizer in the rate of drug metabolism, by preparing a DNA sample from a dog, and determining a base corresponding to a base at position 1117 of a canine CYP1A2 gene (i.e., at position 87 of exon 4). According to the method, a CYP1A2 gene diagnosis of dogs (particularly beagles) used in a pharmacological effect test or a toxicity test can be rapidly carried out prior to the test, and thus the dogs can be easily divided into a group having a normal metabolic ability (an extensive metabolizer group) and a group having a low metabolic ability (a poor metabolizer group).